CenCore version 5.1.3 Papyright (c) 1993 - 2003 Compugen Ltd

protein search, using sw model OM protein January 16, 2003, 16-39,12 , Seatch time 7,28571 Seconds (Without alignments) 28-464 Million rel! updates/sec Run on:

US-09-856-070-16 25 1 EREKE 5 litle: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satistying chosen parameters: 112892 seqs, 41476328 residues

112892

Minimum DB seq length: 0 Maximum DB scq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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While O., Hickey E.K., Peterson J. Hiterback T., Barry K., Bass S.,
Linber K., Weidman J., Khouri H., Craven B., Powann C., Podson P.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
                                       Caps
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HEQUINGTON: HINDS SPECIFICALIZ TO THE SSRA RNA (IMRNA) AND IS REQUIRED FOR STABLE ASSOCIATION OF SSRA MITH RIBOSOMES (BY
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100.0%; Secre 25; DB 1, Length 85,
100.0%; Prod. No. 39;
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                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae (Chlamydophila pneumoniae).
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30-MAY-2000 (Rel. 39, Created)
80 MAY-2000 (Rel. 39, Last Sequence update)
16-0CF-2001 (Rel. 40, Last annotation update)
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EMBL; AP002546; BAA98547.1; -.
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                                       5; Conservative
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                    Best Local Similarity
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-!- SUBGNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHILH PROTEIN. FORMS HOMO-OF HETERO-OLIGOMERS WITH MYOGENIN, ELLA AND ITEP PROTEINS (HY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear.
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CLASS A SPECIFIC ROMAIN.
35138AF36552600C CRC64:
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Xenopus Laevis (African clawed frog).
Eukaryota, McCaroa, Chordata, Cranidta, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of non-tissue-specific helix-loop-helix qenes in Xenopus lacvis.";
Gene 165:319-320(1995).
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                                                     151 AA; 17449 MW; 01D229CA79F7F562 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       F.K.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96096542; PubMed-8522197;
PROSITE; PS01317; SSRP; 1. RNA binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001092; HLH_basic.
PIAM; PF00010; HLH; 1.
SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 125
152 AA: 17455 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00038; HLH_1; 1. PROSITE; PS50888; HLH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSCRIPTION FACTORS.
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.(
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U25959; AAA92047.1;
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shain D.H., Zuber M.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                      135 EREKE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 EREKE 47
                                                                                                                                                                                                                   1 EREKE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EREKE 5
                                                                                                                                                                                                                                                                                                                                                                                                          HIFF XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUM-Head;
                                                        SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                   Levi A., Nasi S.,
"Interplay of the E box, the cyclic AMP response element, and
"Interplay of the E box, the cyclic AMP response element, and
HTF4/HIBB in transcriptional regulation of the neurospecific,
neurotrophin-inducible vgf gene.",
Mol. Cell Hiol 17-1244-1253(1997)
-!- FUNCTION: HINIS SPECIFICALNY TO OLIGOMEKS OF E-BOX MOTIFS, AND IN
PARTICILLAR THE VIEW PRIVANTER E-BOX MAY IMPORTANT POLICE PURPLY
DEVELORMENT OF THE NERVOUS SYSTEM AS WELL, AS IN OTHER ORGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ITE2 PROTEINS (BY SIMILARITY).
SUBCELLULAR LOGATION: Northal SIMILARITY: RELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBBINITY EFFICIENT ON HINDING REQUIRES DIMPRIZATION WITH ANOTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BHLH PROTEIN, FORMS HOMO- OR HETERO-OLICCMERS WITH MYGGENIN, E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELLIX-LOOP-HELLX MOTIF (BY SIMILARITY). CLASS A SPECIFIC DOMAIN. 4R7D037A19AFA395 CPC64;
                                                                    30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transcription factor 12 (Transcription factor HTF-4) (E-box-binding
                                                                                                                                                                                                                                                                                                                              di Rocco G., Pennuto M., Ilii R., Canu N., Filocamo G., trani E.,
Rinaldi A.M., Possenti R., Mandolesi G., Sirinian M.I., Jucker R.,
                                                                                                                                                                Papio hamadryas (Hamadryas baboon).
Ebkarysta, Medabaa, Chesdata, Cramiata; Vertebrata, Enteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DR 1, Length 160;
100.0%; Pred, No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Franscription regulation; DNA-binding; Nuclear protein;
                                                                                                                         protein) (DNA-binding protein HTF4) (Fragment).
TCF12 OR HTF4.
                   160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA
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                                                                                                                                                                                                                                                                                                              MEDLINE-97184449; PubMed-9032251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X97234; CAA65873.1; -.
Interpro: IPR001692; HLH_basin
Pfam; PF00010; HLH; 1.
                                                    30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 AA; 18301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE: PS50888; HLH_1; 1. PROSITE: PS50888; HLH_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSCRIPTION FACTORS.
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                   STANDARD;
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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68
110
                                                                                                                                                                                                                                          NCB1_Tax1D: 9557;
                                                                                                                                                                                                                                                                                                TISSUE=Lymphoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 EREKE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EREKE 5
                 HTF4_PAPHA
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ID ATPF_E
HTF4_PAPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an chail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -: - SÜBÜNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBEANE FEGION CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHAGA3, BETA'S, GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. -: - SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
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-1- CATALYTIC ACIIVITY: ATP + H(2)O + H(+)(In) - ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APG-1994) to the EMBL/GenBank/DDBJ databases. 
 : CATALYIIC ACTIVITY, AIF + H(2)G + H(1)(In) - AbF + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 1; Length 162;
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                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCB:_TaxiD-1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus PS3 (Thermophilic bacterium PS-3).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 AA; 18588 MW; ACTEBPUSDURICHR CPC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-DUN 2002 (Rel. 41, Last annotion update)
ATP synthase B chain precursor (EC 3.6.3.14).
                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, last sequence update)
12-UN-2002 (Rel. 41, last annotation update)
ATP synthase B chain (EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGREAMS; TIGROTIA4; ATP_SYDt_b; 1.
Hydrogen ion transport, Transmembrane, CF(0).
TRANSMEM 16 36 POTENTIAL.
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Matches 5, Conserva
                                                                                                                                                                                                   Bacillus caldotenax.
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P09221;
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P41014;
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-!- SIMILAPITY. RELONGS TO THE ATPASE B CHAIN FAMILY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIANF-98/96665; PubMed-9537320; Deckert G. Warren P.V. Gaasterland T., Young W.C., Lenex A.L., Creham D.E., Overbeek R., Shead M.A. Keller M. Aujay M., Huber P. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria: Aquificae: Aquificae (class). Aquificales, Aquificaeeae:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 163; 100.0%; Pred. No. 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 167, 100.0%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transmembrane, Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA; 18566 MW; BRE790CAUEF18ACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 167 AA; 2001! MW; A1FA1CF360A64554 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP SYNTHASE B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothelical protein AQ_1581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrogen ion transport; Transmembrane; CF(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Wismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. Au.
                                                                                                                                                                                                                                      or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002146; ATPsynt_B/B'sub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                         Plam; PF00430; ATP-synt_B; 1.
TIGRFAMs; TIGR01144; ATP_synt_b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                      EMBL; X07804; CAA30650.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: AE000746: AAC07489.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
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                                                                                                                                                                                                                                                                                                                                         PIR; S01399; S01399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 EPPKE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Micinformatics and the BMM, outstation the European Bicinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no warmodified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                               Sorokiu A.V., Zumstein E., Azevedo V., Ehrlich S.D., serror P.; "The organization of the Bacillus sublitis 168 chromosome region between the spovA and sorA genetic loci, based on sequence data."
                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thesis (1989), USSR Academy of Sciences, Russia.
                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                       174 AA
                                                                                                                                                  Hypothetical protein ypur (ORFX6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                     MEDLINE-95020538; Pubmed-7934829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L09228; AAA67486.1; -. EMBL; X51510; CAA35883.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Na'ure 390:249-256(1997).
                         STANDARD;
                                                                                                                                                                                                                                                                                                                STRAIN-168 / Marburg;
                                                                                                                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-168 / SHGW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mironov V.N.;
                       YPUF_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-168;
                                                                                                                                                                                                                       Bacteria;
                                           P176\overline{17}
YPUF_BACSU
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us-09-856-070-16.rsp

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Decourse, 18.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficienc, virus type C (isolate NIB-Z) (HIV z).
Viruses, Estroid viruses: Fettroifidae: Lentivirus
NCBI_TaxiD=11719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%, Score 25; DB 1, Length 180, 100.0%; Pred. No. 84; 0, Hidrels
                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 174; 100 0%; Pred No 81;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYRISTATE (BY SIMILARITY).
                                                                                                                                     Hypothetical protein, Cemplete proteche.
SROGENCE 174 AA; 21021 MW; 200690744F0R7FPAB CP064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COURETRABILETERY OPCEA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, 19st annotation appare)
Negative factor (F-protein) (27 kDa protein) (3/ORF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Greated)
01-FEB-1996 (Rel. 33, Last Sequence update)
10-FEB-1996 (Rel. 41, Last annotation update)
ATP synthase B chain (EC 3 6 3 14) (Submit I).
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                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; JO3654; NEF$2NIHZ.
InterPro; IPP001558; HIV_NAf
EMBL; 299116; CAB14255.1; -. PIR; S45548; S45548
Subtilist; BG10523; ypuF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J03654; AAR00762.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oucry Match
Bost Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                Local Similarity 100 o
hes 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 EREKE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EREKE 5
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P48186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEF_HV2NZ
P05860.
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
NEF_HV2NZ
NEF_HV2NZ
ND P0586
DT 001-NO
DT 011-NO
DT 15-JU
DE NEGAT
OS HUMAN
OS NHUMAN
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See Milp.//www.isb-sib -h/announce/
or send an email to license@isb-sib.ch).
                                                            Bukarjota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade;
Paninoideae, Andropoqoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SÜBĞÜLİ: F-IYVE AIFASES BAVE 2 COMPONENIS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBERANE FECTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHGA(3), BETAG(1), DELTA(1), EPSILON(1), CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
SCHCELEULAR LOCATION: Chloroglast thyiakoid membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    transcript editing.";
J. Mol. Biol 251-614-628(1995).
-: CATALYTIC ACTIVITY: ATF + H(2)O + H(+)(in) - ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugarua m.;
"Loss of all rob genes as determined by septemeing the entire chicropast genome of the black pine Pinus thunbergii.";
Proc. Nati Acad. Sci (0.8 A 91.9794-9798(1994)
-1. CAIALVIIC ATIVITY AIF + H(2)Q + H(+)(In) - ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Vizidiplantae, Streptophyta, Emkryuphyta, Tracheophyta,
Spermatophyta, Confferopsida, Conflerales, Pinaceae, Pinus.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDINE-95395841; PubMcd-7666415; MEDINE-95395841; PubMcd-7666415; Maiet R.M., NewErmann K., Igioi G.i., Koessel H.; Gomplete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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MFDLINE-95024047; PubMed=7937893;
Wakasugi T., Tsudzuki T., Ito S., Nakashima K., Tsudzuki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 1; Length 183; 100.0%; Pred No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prime, Provide 10, ATP-synt_B; 1.
Hydrogen ion transport; Transmembrane; CF(0); Chloroplast, TPANSMEM 27 45 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 183 AA; 20981 MW; 3748C901295116CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finus thumbergil (Green Pine) (Gapanese black pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP synthase B chain (EC 3.6.3.14) (Subunit 1).
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11-EET-1998 (Fe) 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002146; ATPsynt_B/B'sub.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X86563, CAA60382-1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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                                   Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_TaxID=3350;
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062939;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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this SWISS PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as to content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ist-sib.eh/announce/
SUBUNII: E TYPE ATDASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL, CF(1) HAS FIVE SUBUNITS: ALPHA(1), BETA(3), GAMAA(1), DELTA(1), EPSILON(1), CF(0) SUBCPITUTAR LOTATION: CHOUCEAST, TBYLARACIA Membrane, SIMILARITY: HELONGS TO THE ATDASE B CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruit C.J., White O., Oisen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Godayne J.D., Kerlavage A.R., Douthberty B.A., Tomb. T. F., Adams M. D. Reich C.L., Sovit J. L., Geoghagen N.S.M., Weldman J.E., Pubrmann J.L., Nauyen D., Ufferback H.K., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hust M.A., Naine B.P., Rondovsky M., Klenk H.P., France C.M., Smith H.O., Wocse C.R., Venter J.C., Complete genome sequence of the methanogenic archaeon, Methanococus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci, Methanococcales,
Methanocaldococcaceae; Methanocaldococcus.
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40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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MEDLINE-96437999; PubMcd-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR002146; ATPsynt_B/B'sub.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ptam; PF00430; ATP-synt_B; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D17510; BAA23471.1;
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Matches 5, Conservative
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P54020;
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the European Hointormatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no will modified and this statement is not removed. Usage by and lor commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license*Isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                      SIMILARITY: COMTAINS 1 S4 RNA-BINDING DOMAIN.
SIMILARITY: BELONGS TO THE S4P FAMILY OF RIBOSOMAL PROTEINS.
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!- FUNCTION: IHIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA

(BY SIMILARITY).

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Matches
            EMBL; 067475; AAH98170.1; ·.
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FUNCTION. GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropoda, Mandibulata, Panerustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF HEAD STRUCTURES (HY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear (Hy similarity).
-!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC
                                                                                                                                                                                                                :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haker R.H., Desaile R.; "Multiple sources of character information and the phylogeny of Hawaiian Drosophilids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
O
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                                                                                                                                                                               DB 1; LCD4th 187;
                                                                                                                                                                                                                0; Indels
                                                                                   HGRPAMS; TIGRO1018; rpsD_arch; 1.
PROSILE; rsvu612; RIBOSOMAL_S4; 1.
Ribosomal protein; IRNA-binding; Complete profeome.
BOMAIN 105 RNA-BINDING (S4 TYPE).
SEQUENCE 187 AA; 22050 MW; 7040513899580812 CMC64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase: FBas0023622; Dsil\hb.
Developmental protein: Gap protein; Zinc-linger;
                                                                                                                                                                                                                                                                                                                                                                                            40, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 196 AA
                                                                                                                                                                               100.0%: Secre 25; DB 100.0%; Pred. No. 88;
                                                                                                                                                                                                           0; Mismat.ches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
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POLY-GLN.
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                          InterPro: IPR001912; Ribosomal_S4.
InterPro: IPR002942; S4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila silvestris (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                        045255; 046257;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                          Hunchback protein (Fragments).
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                                                                                                                                                                                               100.08;
                                                                                                                                                                                                             5; Conservative
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                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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81
103
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132
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                                                                                                                                                                                               Best Local Similarity
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HSSP; P81288; 1G05.
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es 5; Conserv
                                                       Plam; PF01479; S4;
SMART; SM00363; S4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-47010;
                                                                        SM00363;
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102
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25 EREKE 29
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caps
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PROSITE; PS00715; SIGMA70_2: 1
Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
DNA-binding; Sporulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN+HD-1-Dippel;
MPDFINE-9126763;
Adams L.F., Bryon K.L., Whiteley H.R.;
"Molecular cioning and characterization of two genes encoding sigma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA POLYMERASE SIGMA-LB FATTOP
POLYMERASE CORE BINDING (POTENTIAL).
H-T-H MOTIF (HY SIMILARITY).
CIDBRAEB637CEDA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factors that direct transcription from a Bacilius thuringiensis crystal protein gene promoter.",
J. Bacterioi 173:3846-3854(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                   P26765;
01-80(-1992 (Rel. 23, Created)
01-80(-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Mismatches
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177 FRFKE 181
                                                                                                                                                                                                                                       RP28_BACTK
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TickFams; TifkFulls; 1.
PROSITE; PSOI127; EF_TS_1; 1.
PROSITE; PSOI127; EF_TS_2; 1.
Elongation factor; Protein blosynthesis.
SILE 82 85 TUVOSVED IN MG: 10N DISLOCATION FROM EF-TO REPORTED FROM FROM EF-TO REPORTED FROM EF-TO REPORTED FROM FROM EF-TO REPORTED FROM EFFT.
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Sanangelantoni Δ M , Calogero R C , Buttarelli F R , Gualerzi C O
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247 AA; 25897 MW; BDFESE82198871ED CRC64;
                                                                                                                                                                                                                                                                                                                              Borteria: Cyanobacteria; Oscillatoriales; Spirulina.
NCBL_TaxID-1156;
                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Fel. 28, Last Seyuence update)
16-CFC-2001 (Rel. 40, Last annotation update)
Flougation factor is (FF-Is) (Frequent).
    247 AA.
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Pfam; PF00627; UBA; 1.
Pfam; PF00889; EF_TS; 1.
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EFTS_SPIPL
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